

1/24

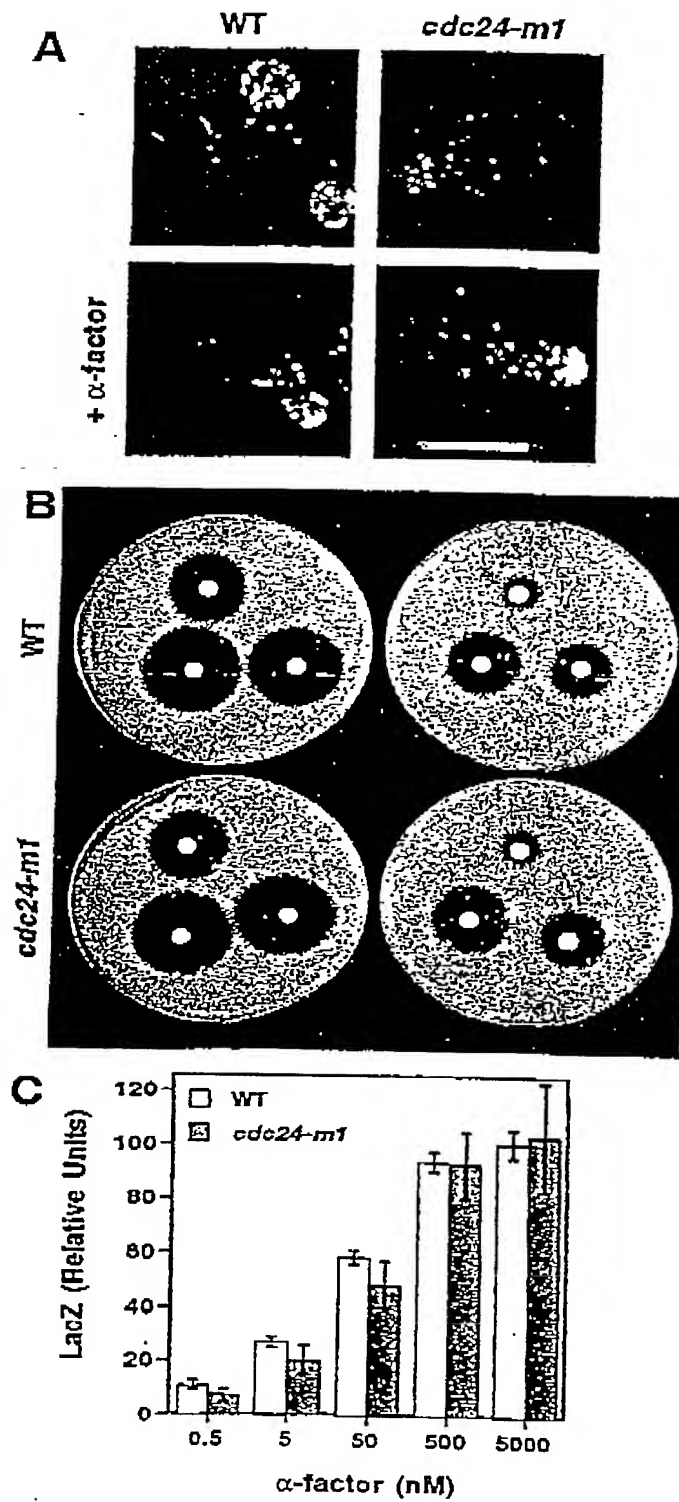


FIG. 1

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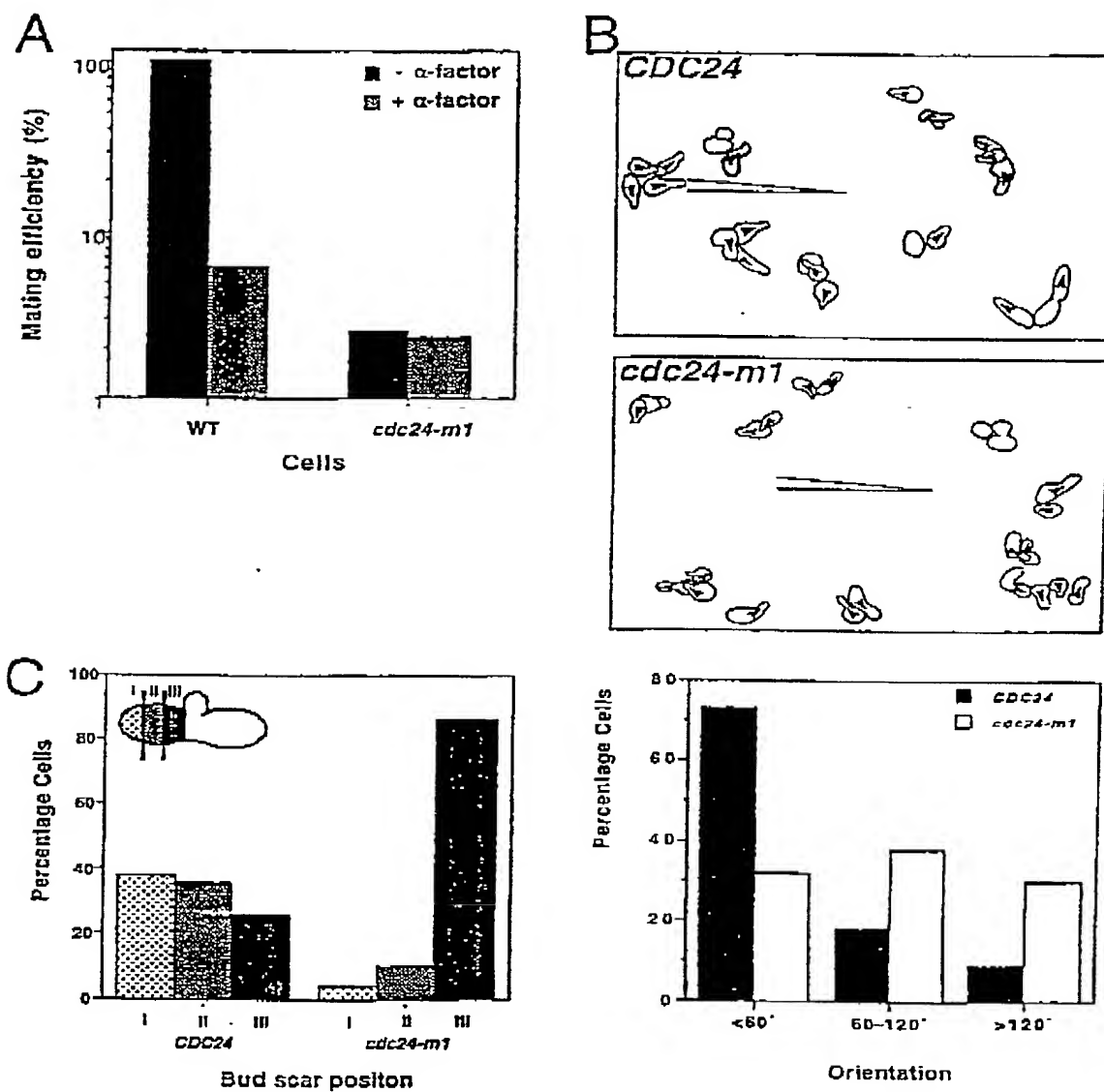


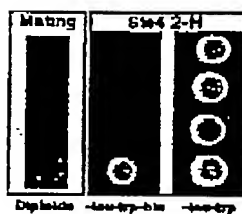
FIG. 2

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A

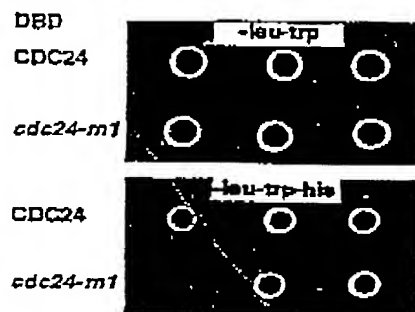
Cdc24-m1	QFKLPVIAFDRLRVCKKSI
Cdc24-m2	QFKLPVIASGDLRVCKKSI
Cdc24-m3	QFKLPVIAFDRLRVCKKSI
Cdc24 Sc	181 QFKLPVIASDRLRVCKKSI 189

Dhl Hu	335 QYEFDVILSPDLKVGKRTI 403

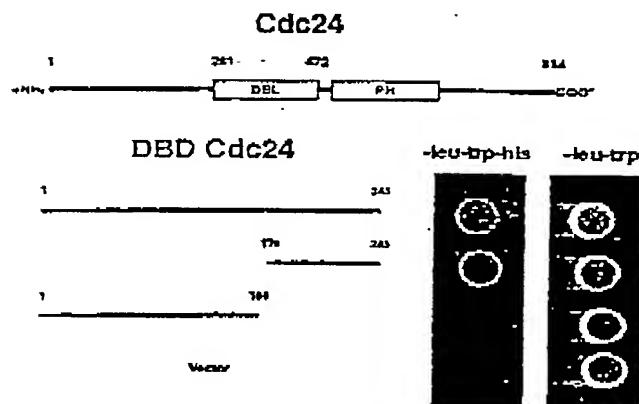


B

AD STE4 CDC42 BEM1



C



D

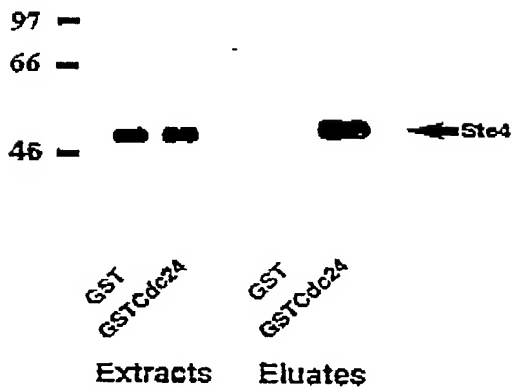


FIG. 3

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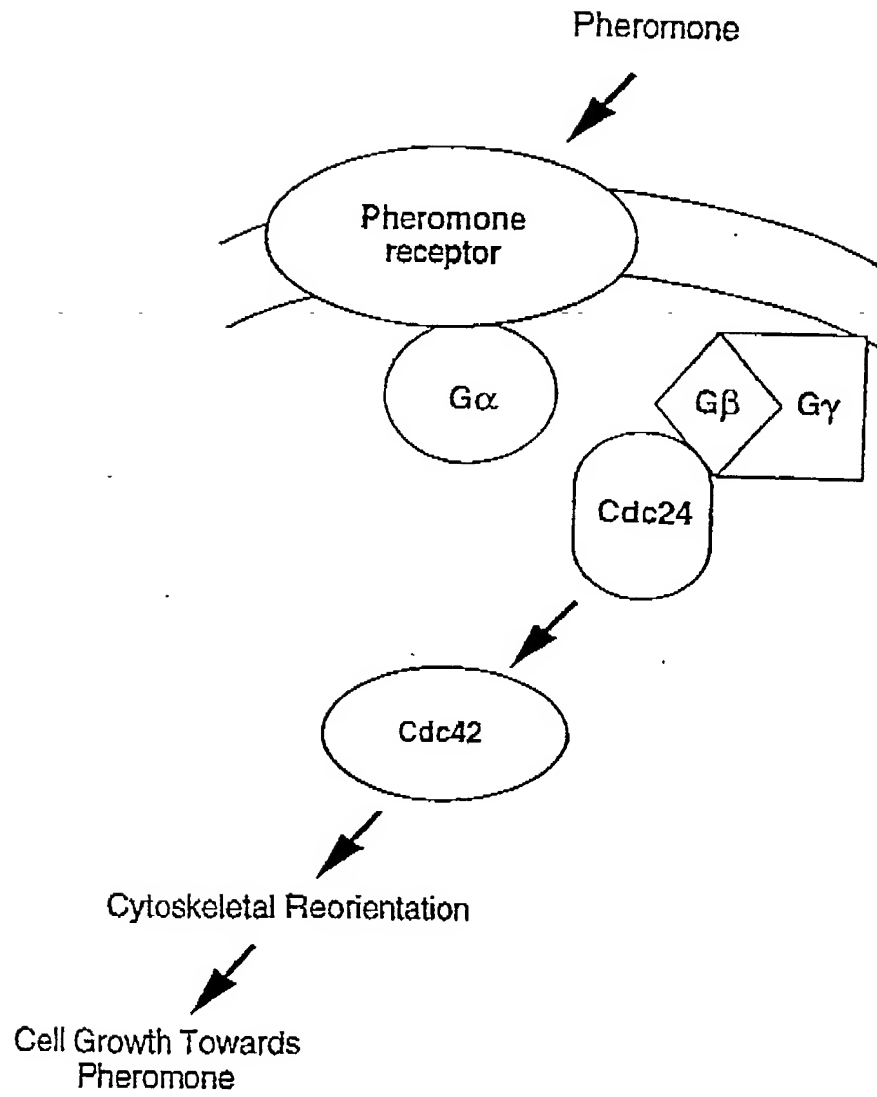


FIG. 4

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Figure 5

5 2113/1
ATG GAA CAT CCA CCA GCA GCT CTC AGA ACA TTT TCA ACC CAA TCA ACT TCA TCT TTG AAT
M E H P P A A L R T F S T Q S T S S L N

10 2173/21
TCA GTA AGT ACT GTT TCG TCT TCA AGA ATT GTT TCT CTG GGC CCA GTC AAT ATA AAC AAT
S V S T V S S S R I V S S G P V N I N N

2233/41
TTC AAT AAA CCA AGT ACT CCC AAA GAC CAT TTA TTC TAT CGA TGT GAA TCA CTA AAA CGA
F N K P S T P K D H L F Y R C E S L K R

15 2293/61
AAA CTA CAA AAA ATC CCT GGC ATG GAA CCA TTT TTG AAC CAA GCT TTC AAT CAG GCT GAA
K L Q K I P G M E P F L N Q A F N Q A E

2353/81
CAA CTC AGT GAA CAA CAA GCA TTG GCT TTG GCA CAG GAA AGA AGC AAT GGA AAT GGA CAT
Q L S E Q Q A L A L A Q E R S N G N G H

20 2413/101
AGT AAT GGC AAA CGT CAT CAA TCA TTA GAC GGT GCC ATG AAT AGA CTT TCA GTT GGT TCT
S N G K R H Q S L D G A M N R L S V G S

2473/121
GAT AGT AGT TCG ATC CAA GGT TCA TTG ACA CGA ATG GCC ACC AAT GCG TCA ACG TCA TCT
D S S S I Q G S L T R M A T N A S T S S

25 2533/141
TTA ATC AGT GGT ATG CCA AAC AAC AAC ACT TTA TTT ACG TTT ACT GCA GGG GTT TTA CCA
L I S G M P N N N T L F T F T A G V L P

30 2593/161
GCT AAT ATT AGT GTC GAT CCT GCT ACC CAT CTT TGG AAA TTG TTC CAA CAA GGG GCC CCC
A N I S V D P A T H L W K L F Q Q G A P

2653/181
TTT TGT GTT CTT ATC AAT CAT ATC CTT CCT GAT TCC CAA ATA CCA GTT GTC AGT TCT GAT
F C V L I N H I L P D S Q I P V V S S D

35 2713/201
GAC TTG AGA ATT TGC AAA AAA TCA GTA TAT GAC TTT TTA ATT GCC GTC AAG ACA CAA TTG
D L R I C K K S V Y D F L I A V K T Q L

2773/221
AAT TTT GAT GAC GAG AAT ATG TTC ACT ATA TCC AAT GTT TTC TCC GAC AAT GCC CAA GAT
N F D D E N M F T I S N V F S D N A Q D

40 2833/241
TTA ATC AAG ATT ATT GAT GTC ATT AAT AAA CTA CTT GCT GAG TAC TCA GAT GCT AGT GAC
L I K I I D V I N K L L A E Y S D A S D

45 2893/261
CTG GGT GGT GGC GAT GAA GAT GTA AAT ATG GAT GTT CAA ATT ACC GAT GAA AGA TCA AAA
S G G G D E D V N M D V Q I T D E R S K

2953/281
GTT TTC CGA GAA ATT ATC GAA ACA GAA AGA AAT TAT GTT CAA GAC TTG GAA CTA ATG TGT
V F R E I I E T E R K Y V Q D L E L M C

50 3013/301
AAA TAC CGT CAA GAT CTA ATT GAA GCC GAA AAT TTG TCT TCA GAA CAA ATT CAC TTG TTA
K Y R Q D L I E A E N L S S E Q I H L L

3073/321
TTC CCA AAT TTA AAT GAG ATT ATT GAT TTT CAA AGA CGA TTC CTC AAT GGG TTA GAA TGT
F P N L N E I I D F Q R R F L N G L E C

55 3133/341
AAC ATC AAT GTA CCT ATT AGA TAT CAA AGA ATT GGA TCA GTA TTT ATT CAT GCT TCT TTG
N I N V P I R Y Q R I G S V F I H A S L

60 3193/361
GGC CCT TTC AAT GCT TAT GAA CCT TGG ACT ATA GGA CAA TTG ACG GCG ATT GAT TTG ATC
G P F N A Y E P W T I G Q L T A I D L I

3253/381
AAC AAA GAA GCT GCT AAT TTG AAA AAA TCG TCA AGT CTA CTT GAT CCT GGG TTT GAA CTT
N K E A A N L K K S S S L L D P G F E L

65 3313/401
CAA TCG TAT ATA TTA AAG CCG ATC CAA AGA TTG TGT AAA TAC CCA CTT TTG TTG AAA GAG
Q S Y I L K P I Q R L C K Y P L L L K E

3373/421
TTA ATC AAA ACA TCA CCA GAA TAT TCA AAA CAG GAC CCC CAT GGC AGC TCG TCA TCG ACA
L I K T S P E Y S K Q D P H G S S S S T

70 3433/441
TCA TTC AAT GAA TTA TTG GTG GCT AAA ACT GCA ATG AAA GAA TTG GCA AAT CAA GTC AAT
S F N E L L V A K T A M K E L A N Q V N

3463/451

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3493/461
 GAG GCG CAA AGA CGA GCA GAA AAT ATC GAA
 E A Q R R A E N I E
 3553/481
 5 AAT TGG CGT GGG TTT AAT TTG GAT GCT CAA
 N W R G F N L D A Q
 3613/501
 GTT AAA GAT GCT GAA AAT GAA AAG GAA TAC
 V K D A E N E K E Y
 10 3673/521
 TTT TTC ACA GAA ATT GAT GAT ACC AAA AAA
 F F T E I D D T K K
 3733/541
 TCG ACA AGA AAG AGA TCA ACT TCA TCA AAT
 S T R K R S T S S N
 15 3793/561
 TCA ATA AAC AAT TCC CGA AAG GAT AAC ACA
 S I N N S R K D N T
 3853/581
 20 ATA TCG GAG ATT TAT AAC ATT TCC GCA CCA
 I S E I Y N I S A P
 3913/601
 TGG TCA GGT AGA AAG GAA AGC GGC TCA TTC
 W S G R K E S G S F
 25 3973/621
 AAC CAA TGG GAA AAG TGT TTA CGT GAT TTG
 N Q W E K C L R D L
 4033/641
 AAG AAG TTA CGT GAT TCC GAC CTG TCA TTT
 K K L R D S D S S F
 30 4093/661
 ACG GGT ATT AGT ACG TCA CCA GTC AAT CAA
 T G I S T S P V N Q
 4153/681
 35 GGC TCT CAC AGT TCC CGC CAT CAC TCA TCG
 G S H S S R H H S S
 4213/701
 AGA GTT AAA TCT GGT GAT TTG AGT AGA ATA
 R V K S G D L S R I
 4273/721
 40 AGT AAC AAC TTG AAT GGG TCA CCA AAT ACC
 S N N L N G S P N T
 4333/741
 ACC AAA ACA ATT CCA ACA TTT GAC GTT GCA
 T K T I P T F D V A
 4393/761
 45 TCA GAG CCA TTG ATT GTC AAT GCA CAA ATT
 S E P L I V N A Q I
 4453/781
 50 TCC CAG ATT ATC ACT TCG AAC TTG GTG GCA
 S Q I I T S N L V A
 4513/801
 AAA GAC GAC GAA GGA GAC TTT GTG AAT TTG
 K D D E G D F V N L
 4573/821
 55 GAT ATG TTA ACC AGT GAA GAC TTT TAC CAA
 D M L T S E D F Y Q
 4633/841
 60 GTG TGG GTT TCT TGA
 V W V S *

3523/471
 CAT TTG GAA AAA CTA AAA GAA AGA GTA GGT
 H L E K L K E R V G
 3583/491
 GGA GAA CTA TTA TTC CAC GGA CAA GTT GGG
 G E L L F H G Q V G
 3643/511
 GTT GCT TAT CTT TTT GAA AAA ATC GTA TTT
 V A Y L F E K I V F
 3703/531
 TCT GAT AAA CAG GAA AAG AAG AGC AAG TTT
 S D K Q E K K S K F
 3763/551
 CTT AGT TCA TCG ACT ACT AAT TTG TTG GAA
 L S S S T T N L L E
 3823/571
 TTG CCA TTG GAA TTA AAG GGA AGA GTT TAT
 L P L E L K G R V Y
 3883/591
 AAC ACT CCT GGC TCA ACT CTA ATC ATC TCA
 N T P G S T L I I S
 3943/611
 ACT TTG AGA TAT CGT AGT GAA GAA GCC AGA
 T L R Y R S E E A R
 4003/631
 AAG ACT AAT GAA ATG AAT AAA CAA ATT CAT
 K T N E M N K Q I H
 4063/651
 AAT ACT GAT GAC TCT GCC ATA TAT GAT TAC
 N T D D S A I Y D Y
 4123/671
 TCA ACT CAA CAA CAA TAC TAT GAT CAT CGG
 S T Q Q Q Y Y D H R
 4183/691
 TCA TCC ACT TTG AGT ATG ATG AAG AAT AAT
 S S T L S M M K N N
 4243/711
 TCT TCA ACT TCA ACA ACA TTA GAT TCT TTC
 S S T S T T L D S F
 4303/731
 ACT AAT CCA TCT TTG ATG TCT TCA GAT GCC
 T N P S L M S S D A
 4363/751
 ATT AAA TTG CTT TAC AAA TCG ACA GAA TTG
 I K L L Y K S T E L
 4423/771
 GAG TAT AAT GAC CTT TTA CAG AAA ATT ATC
 E Y N D L L Q K I I
 4483/791
 GAT GAT GTC AAT ATT AGT CGA TTG AGA TAT
 D D V N I S R L R Y
 4543/811
 AAT TCA GAT GAT GAT TGG GGG TTA GTG CTT
 N S D D D W G L V L
 4603/831
 ACA TCA AGC AAT GAA AAA CGA CTG GTG ACA
 T S S N E K R S V T

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Figure 6

5 Blastp line up of S.c. Cdc24p and C.a. Cdc24p

S.c. Cdc24p: 1 MAIQ---TR-FA 8
M R F+

10 C.a. Cdc24p: 1 MEHPPAALRTFSTQ 14

S.c. Cdc24p: 9 SGTSLSDLKPKPSATSISIPMQNV--MNKPVTEQDSLPHICANIRKRLEVLPOLKPFLLQL 66
S +SL+ + S+ +S N+ NKP T +D LF+ C +++++L+ +P ++PFL

C.a. Cdc24p: 15 STSSLNSVSTVSSSRIVSSGPVNINNFNKPSTPKDHLFYRCESLKRKLQKIPGMEPFLNQ 74

15 S.c. Cdc24p: 67 AYQSSEVLSEKQSLLLSOKQHQELLSKNGANRDSLDAP--TLRSSISISTATSLMSMEG 123
A+ +E LSE+Q+L L+Q++ SNG S D A ++ S S S SL M

C.a. Cdc24p: 75 AFNQAEQLSEQQALALAQERSNGNGHSGNGKRHQSILGAMNRLSVGSDSSSIQGSILTRMAT 134

20 S.c. Cdc24p: 124 ISYTSNPSATPNMEDTLTLTFSMGILPITMDCDPVTQLSOLFQOGAPLCILFNSVKPFQK 183
+ T+S S PN +TL TF+ G+LP + DP T L +LFQOGAP C+L N + P +

C.a. Cdc24p: 135 NASTSSLISGMPN--NNTLFTFTAGVLPANISVDPATHLWKLFFQOGAPFCVLINHLIPDSQ 193

S.c. Cdc24p: 184 LPVIASDDLKVKCKSIYDFILGCKKHFAFNDEELFTISDVFNASTEQLVKVLEVVETLMN 243
+PV++SDDL++CKKS+YDF++ K F+DE +FTIS+VF+++ L+K+++V+ L+

25 C.a. Cdc24p: 194 IPVVSSDDLRIKCKSVYDFLIAVKTQLNFDDENMFTISNVFSDNAQDLIKIIDVINKLLA 253

S.c. Cdc24p: 244 SSPTIFPSKSKTQQIMNAENQHRHQPPQSSKKHNEYVKIIEKFVATERKYVHDLEILDKY 303
S + + + +E K+ +E + TERKYV DLE++ KY

30 C.a. Cdc24p: 254 EYSDASDSGGGDEDV-----NMDVQITDERSKVFREIETERKYVQDLELMCKY 302

S.c. Cdc24p: 304 RQQLDSNLITSEELYMLFPNLGDAIDFQRRFLISLEINALVEPSKQIRIGALFMH-SKHF 362
RQ L+++ ++SE++++LFPNL + IDFQRRFL LE N V ORIG++F+H S

C.a. Cdc24p: 303 RQDLIEAENLSSEQUIHLLFPNLNEIIDFQRRFLNGLECNINVPRIYQIRIGSVFIHASLGP 362

35 S.c. Cdc24p: 363 FKLYEPWSIGQNAAEFLSLSTLHKMRVDESQRFIINNKLELQSFYKPVQRLCRYPLLVK 422
F YEPW+IGQ AI+ ++ ++ S +++ ELQS++ KP+QRLC+YPLL+K

C.a. Cdc24p: 363 FNAYEPWTIGQLTAIDLINKEAANKKSSS--LLDPGFELQSYILKPIQRLCKYPLLK 419

40 S.c. Cdc24p: 423 ELLAE-----SSDDNNTKELEAALDISKNIARSINENQRRTENHQVVKLYGRV 471
EL+ SS + EL A K +A +NE QRR EN + ++KL RV

C.a. Cdc24p: 420 ELIKTSPEYSKQDPHGSSSTSFNELLVAKTAMKELANQVNEAQRRAENIEHLEKLERV 479

S.c. Cdc24p: 472 VNWKGYRISKFGELLYFDKVFISTNSSSEPEREFVYLFEKIILFSEVVTKKSASSLI 531
NW+G+ + GELL+ +V + +E E+E+ YLFEKI+ F+E+ K +

45 C.a. Cdc24p: 480 GNWRGFNLDAQGELLEFGQVGV---KDAENEKEYVAYLFEEKIVFFTEIDDTKKSQKQE 535

S.c. Cdc24p: 532 LKKKSSSTASISASNITDNNGSPHSHYKRRHSNSSSSNNIHLSSSSAAAIHSSSTNSSDN 591
K K ST ++SN+ SSS ++ S NS +

50 C.a. Cdc24p: 536 KKSKESTRKRSTSSNL-----SSSTTNLLESINNSRKD 568

S.c. Cdc24p: 592 NSNNSSSSSLFKLSANEPKLDLGRIMIMNLNQIIPQN--NRSINITWESIKEQGNFLK 649
N+ L+L+GR+ I + I N +L I+W KE G+P L+

C.a. Cdc24p: 569 NT-----LPELEKGRVYISEIYNISAPNTPGSTLIISWSCRKESGSFTLR 613

55 S.c. Cdc24p: 650 FKNEETRDNWSSCLQQLIHDLKNEQFKARHSSSTSTSS-----TAKSSSMSPSTTT 701
+++EE R+ W CL+ L + N+Q + S S+ ++ T S+S ++ +T

C.a. Cdc24p: 614 YRSEEARNQWEKCLRDCLKTNEMNKQIHKKLRDSDSSEFNTDDSAIYDYTGISTSPVNQSTQ 673

60 S.c. Cdc24p: 702 MNTPNHNSRQT--HDSMASFSSSHMKRVS----DVLPRKRTTSSSESEIKS----- 748
+H S + H S ++ S RV + TT SF + +

C.a. Cdc24p: 674 QQYDHRGSHSSRRHSSSSTLSMMKNRVKSGDLSRISSTSTTLDSFSNNLNGSPNTTNP 733

S.c. Cdc24p: 749 --ISENFKNISIPESILFRISYNNNSNNTSSSEIFILLVEKVVNFDDLIMAINSKI--SN 804
+S + +IP + ++ Y +T SE L+V ++DL+ I S+I SN

65 C.a. Cdc24p: 734 SLMSSDATKTIPTDVAIKLLY---KSTELSE--PLIVNAQIEYNDLLQKIIISQIITSN 787

S.c. Cdc24p: 805 THNNNISPIKIKYQDEGDGVVLGSDSDWNVAKEMLAENNEKFLNIRLY 854
++++ I++++Y+D++GDFV L SD+DW + +ML + F +

C.a. Cdc24p: 788 LVADDVN--ISRLRYKDEGDGVVNLNSDDDWGLVLDMLTSED--FYQTSSEKRSVTVVWS 844

70

Figure 7a

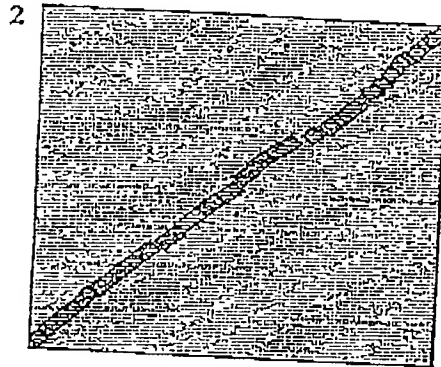
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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix: 0.BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.0 wordsize: 3 Filter ☐ Align ☐

Sequence 1 lcl|S.c. Cdc24p Length 854 (1..854)

Sequence 2 lcl|C.a. Cdc24p Length 844 (1..844)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 446 bits (1136), Expect = e-124

Identities = 288/881 (32%), Positives = 464/881 (51%), Gaps = 112/881 (12%)

```

Query: 9  SGTSLSDLKPKPSATSISIPMQNV--MNKPVTEQDSLPHICANIRKRLVLPQLKPFLLQL 66
      S +SL+ + S+ +S N+ NKP T +D LF+ C +++++L+ +P ++PFL
Sbjct: 15 STSSLNSVSTVSSSRIVSSGPVNINNFNKPSTPKDHLFYRCESLKRKLQKIPGMEFFLNQ 74

Query: 67 AYQSSEVLSEKQSLLSQKQHQELLKSNGANRDSDDLAP---TLRSSSISTATSLMSMEG 123
      A+ +E LSE+Q+L L+Q++ SNG S D A ++ S S S SL M
Sbjct: 75 AFNOAEQLSEQQALALAQERSNGNGHNSNGKRHQSLDGAMNRLSVGSDSSSIQGSILTRMAT 134

Query: 124 ISYTNNSNPATPNMEDTLTFSMGILPITMDCDPVTQLSQLFQQGAPLCILFNSVKPQFX 183
      + T+S S PN +TL TF+ G+LP + DP T L +LFQQGAP C+L N + P +
Sbjct: 135 NASTSSLISGMPN--NNTLFTFTAGVLPANISVDPPATHLWKLFFQQGAPFCVLINHILPDSQ 193

Query: 184 LPVIASDDLKVCKKSTYDFILGCKKHFAFNDEELFTISDVFNSTSQLVKVLEVVEITLMN 243
      +PV++SDDL++CKKS+YDF++ K F+DE +FTIS+VF+++ L+K+++V+ L+
Sbjct: 194 IPVSSDDLRIKKSVDYDFLIAVKTQLNFDENMFTISNVFSDNAQDLIKIIDVINKLLA 253

Query: 244 SSPTIFPSKSKTQQIMNAENQERHQPPQSSKKHNEYVKIIEFVATERKYVHDLEILDKY 303
      S + + + +E K+ +E + TERKYV DLE++ KY
Sbjct: 254 EYSDASDSGGGDEDV-----NMDVQITDERSKVFREIITERKYVQDLELMCKY 302

Query: 304 RQQLLDSNLITSEELYMLFPNLGDAIDFORRFLISLEINALVEPSKORIGALFMH-SKHF 362
      RQ L+++ ++SE++++LFFNL + IDFORRFL LE N V ORIG++F+H S
Sbjct: 303 RQDLTEAENLSSEQIHLLFPNLNEIIDFORRFLNGLECNINVPYRIGSVFIHASLGP 362

Query: 363 FKLYEPWSICQNAAYEFLSSTLHKMRVDESQRFIINNKLELQSFLYKPVQRLCRYPLLVK 422
      F YEPW+IGQ AI+ ++ ++ S +++ ELQS++ KP+QRLC+YPLL+K
Sbjct: 363 FNAYEPWTIGQLTAIDLINKEAANLKKSSS---LLDPGFELQSYILKPIQLCKYPLLLK 419
  
```


F Figure 7a cont.

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Query: 423 ELLAE-----SSDDNNTKELEAALDISKNIARSINENQRRTENHQVVKKLYGRV 471
 EL+ SS + EL A K +A +NE QRR EN + ++KL RV
 Sbjct: 420 ELIKTSPEYSKQDPHGSSSSSTSPNELLVAKTAMKELANQVNEAQRRAENTIEHLEKLERV 479

Query: 472 VNWKGYRISKFGELLYFDKVFISTTNSSSEPEREFVYLFEKIILFSEVVTKKSASSLI 531
 NW+G+ + GELL+ +V + +E E+E+ YLFEKI+ F+E+ K +
 Sbjct: 480 GNWRGFNLDAQGELLFHGQVGV----KDAENEKEYVAYLF EKIVFFFTTEIDDTKKSDKQE 535

Query: 532 LKKKSSTASISASNITDNNGSPHSHYKRRHSNSSSSNNIHLSSSSAAATIHSSSTNSSDN 591
 K K ST ++SN+ SSS ++ S NS +
 Sbjct: 536 KKSSTSTRKSTSSNL-----SSSTTNLLESINNSRXD 568

Query: 592 NSNNSSSSSLFKLSANEPKLDLRGRIMIMNLNQIIPQN--NRSLNITWESIKEQGNFLK 649
 N+ L+L+GR+ I + I N +L I+W KE G+F L+
 Sbjct: 569 NT-----LPLELKGVRVYISEIYNISAPNTPGSTLIISWSCRKESGSPTLR 613

Query: 650 FKNEETRONWSSCLQQLIHDLKNEQFKARHHSSTSTSS-----TAKSSSMMSPPTT 701
 +++2E R+ W CL+ L + N+Q + S S+ ++ T S+S ++ +T
 Sbjct: 614 YRSEEARNQWEKCLDLKTNEMNKQIHKKLRDSDSSFNTEDDSAIYDYTGISTSPVNQSTQ 673

Query: 702 MNTPNHHNSRQT--HDSMASFSSSHMKRVS----DVLPRKRTTSSSPFESEIKS----- 748
 +H S + H S ++ S RV + TT SF + +
 Sbjct: 674 QQYYDHRGSHSSRHSSSSTLSMMKNRVKSGDLSRISSTSTTLDSFSNNLNGSPNTTNP 733

Query: 749 --ISENFKNISIPESILFRISYNNNSNNTSSSEIFTLLVEKVWNFDDLIMAINSKI--SN 804
 +S + +IP + ++ Y +T SE L+V ++DL+ I S+I SN
 Sbjct: 734 SLMSSDATKTIPTFDVAIKLLY----KSTELSE--PLIVNAQIEYNDLLQKIISQIITSN 787

Query: 805 THNNNISPIKIKYQDEDDGDFVVLGSDDEDWNVAKEMLAENN 845
 ++++ I++++Y+D++GDFV L SD+DW + +ML +
 Sbjct: 788 LVADDVN-ISRLRYKDDGDFVNLNSDDDDWGLVLDMLTSED 827

CPU time: 0.26 user secs. 0.02 sys. secs 0.28 total secs.

Gapped
 Lambda K H
 0.270 0.0470 0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 12253

Number of Sequences: 0

Number of extensions: 709

Number of successful extensions: 15

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 844

length of database: 90,077,593

effective HSP length: 63

effective length of query: 781

effective length of database: 83353792

effective search space: 65099311552

effective search space used: 65099311552

r: 9

A: 40

X1: 16 (7.2 bits)

X2: 128 (49.9 bits)

X3: 128 (49.9 bits)

S1: 42 (21.9 bits)

S2: 73 (32.8 bits)

Figure 7b

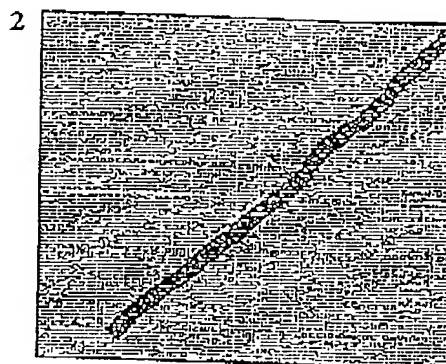
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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

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 x_dropoff: 50 expect: 10.0 wordsize: 3 Filter ☐ Align

Sequence 1 lcl|S.c. Cdc24p Length 854 (1..854)

Sequence 2 lcl|S.p. Cdc24p Length 834 (1..834)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 238 bits (601), Expect = 1e-61
 Identities = 212/760 (27%), Positives = 348/760 (44%), Gaps = 94/760 (12%)



Query: 156 DPVTQLSQLFQQGAPLCILENSVKPQPKLPVIASDDLK---VCKKSIYDFILGCKKKHFAF 212
 DPVT++ + G PLC LEN + + KL V +S L+ VCK S+Y F+L CK
 Sbjct: 67 DPVTEIWLFCRLGYPLCALFNCLFVKQKLEVNSSVSLENTNVCKASLYRFMLMCKNELGL 126

Query: 213 NDEELFTISDVFANSTSQLVKVLEVETLMNSSPTIFPSKSKTQQIMNAENQERHQPQQS 272
 D LF+IS+++ ST+ LV+ L+ +E L+ +KS + + + S
 Sbjct: 127 TDAALFSISEIYKPPSTAPLVRALQTIELLLKKYEVSNNTTKSSSTPSPSTDDNVPTGTINS 186

Query: 273 SKKHNEYVKIIEFVATERKYVHOLEILDKYRQQLLDSNLTSEELYMLFPNLGDAIDFQ 332
 ++ E TE KY+ DLE L Y L +-+ + + +F NL + +DFQ
 Sbjct: 187 LIASGR--RVTAELYETELKYIQDLEYLSNYMVILQQKQILSQDTILSIFTNLNEILDQ 244

Query: 333 RRFLISLEINALVEPSKQRIGALFMHSHKHFKLYEPWSIG-QNAAIEFLSSTLHKMRVDE 391
 RRFL+ LE+N + +QR+GALF+ + F +Y+ + .NA + + ++V
 Sbjct: 245 RRFLVGLEMNLSLPVEEQRLCALFIALEEGFSVYQVFCNTNFPNAQQLIIDNQQLLKVAN 304

Query: 392 SQRFIINNKLQLSFLYKPVQRLCRYPLLKELL-AESSDDNNTKELEAALDISKNIARS 450
 ++ EL + L KP+QR+C+YPLL+ +LL S +EL+ + +A
 Sbjct: 305 ----LLEPSYELPALLIKPIQRICKYPLLNLQLLKGTSPSGYQYEEELKQGMACVVRVANQ 360

Query: 451 INENQRRTENHQVVKLYGRVWNWGYRISKFGELLYFDKVPISTNNSSEPEREFEVYL 510
 +NE +R EN + +L RV++WKGY + FG+LL +D V + ++ ERE+ VYL
 Sbjct: 361 VNETARRIHENRNAIIIELEQRVIDWKGYSLOYPGQLLVWDVVNV----CKADIEREYHVYL 416

Query: 511 FEKIIILFSEVVT-KKSASSLILKKKSSTSAS-----ISASNITDN----- 550
 FEKI++ E+ T K+ A S+ + KK+ S I SNIT
 Sbjct: 417 FEKILLCKEMSTLKROARSISMNKKTKRLDSLQKGRILTSNITTVPNNHMGSYAIQI 476

Figure 7b cont.,

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Query: 551 --NGSPHHSYHKRHSNSSSSNNIHL-----SSSAAAIHSSTNSSDNNNSNNSSSS 599
 G P H + S+ + +S + I S+ ++ N N SSS
 Sbjct: 477 FWRGDPQHESFILKLRNEESHKLWMSVLNRLWLKNEHGSFKDIRSAASTPANPVYNRSS 536

Query: 600 SLFKLSANEPKLD-LRGRIMIMNLN---QIIPQNNRSLNITWESIKEQGNFLLKFKNEET 655
 K N D LR + N+N I +++S T + K+ K+ T
 Sbjct: 537 QTSK-GYNSSDYDLLRTHSLDENVNSPTSISSPSSKSPFTKTTSKDT-----KSATT 588

Query: 656 RDNWSSCLOQLIHDLKNEQFKARHHSSTST-----TSSTAKSSSMMSPPTTMMNT--PNHH 708
 D S +L + R +TST +SSTA S +S + +N+ +++
 Sbjct: 589 TDERPSDFIRLNSEESVGTSSLRTSQTSTIVSNDSSSTASIPSQISRISQVNSLLNDYN 648

Query: 709 NSRQTH-----DSMASF---SSSHMKRVSD-----VLPKRRTTSSSPFESE 745
 +RQ+H S++ F SSS +++ D + P++ + S+ +S+
 Sbjct: 649 YNRQSHITRVYSGTDDGSSVSIFEDTSSSTKQKIFDQPTTNDCDVMRPRQYSYSAGMKSD 708

Query: 746 IKSISENFKNSIPESSILFRISYNNNSNNTSSSEI---FTLLVEKVWNFDDLLIMAINSK 801
 + S+ SS +S N +N + L+V FD+L+ + K
 Sbjct: 709 GSLLPSTKHTSLSSSSTSTSLSVRNTTNVKIRLRLEHVSLLVVAHDITFDELLAKVERK 768

Query: 802 IS--NTHNNNISPIKIKYQEDGDGFVVLGSDDEDWNVAKE 839
 I + ++KY DEDGDF+ + SDED +A E
 Sbjct: 769 IKLCGILKQAVPFRVRLKYVDEDGDFITITSDEDVLMFAE 808

CPU time: 0.26 user secs. 0.04 sys. secs 0.30 total secs.

Gapped
 Lambda K H
 0.270 0.0470 0.230

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 10384
 Number of Sequences: 0
 Number of extensions: 671
 Number of successful extensions: 13
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 2
 Length of query: 834
 Length of database: 90,077,593
 effective HSP length: 61
 effective length of query: 773
 effective length of database: 83489227
 effective search space: 64537172471
 effective search space used: 64537172471
 T: 9
 A: 40
 X1: 16 (7.3 bits)
 X2: 128 (49.9 bits)
 X3: 128 (49.9 bits)
 S1: 41 (21.7 bits)
 S2: 73 (32.8 bits)

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Figure 8

5 Sc KLPVIASDDLKVCKKSIYDFIL (SEQ ID No 25)

++PV++SDDL++CKKS+YDF++

Ca QIPVVSSDDLRLCKKSVYDFLI (SEQ ID No 26)

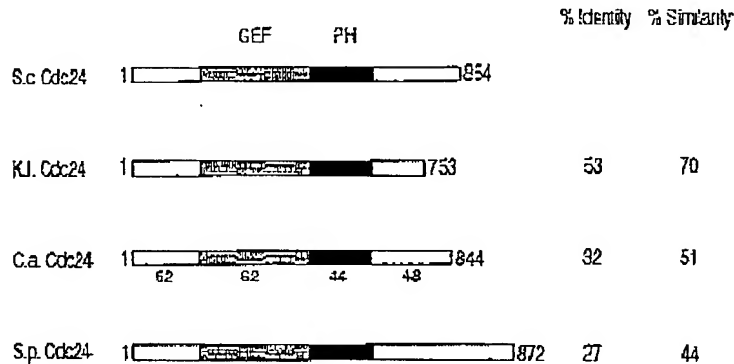
10 Sc = *Saccharomyces cerevisiae*

Ca = *Candida albicans*

A

Fungal Cdc24's

figure 9



B

Guanine nucleotide exchange factor domain of CaCDC24 is homologous to other fungal Cdc24p's

[illegible]

C

Homology of Stc4p binding region

S. c. 170 **D**LCILNN**N**IK**P**Q**E**FL**E**PN**S**ED**L**---VCKKSIYD**P**IL**G**CF**Y**FL**N**DE**E**LS**T**IS**D**VF**N**
 K. l. 164 **P**LC**I**L**I**NA**V**R**P**Q**S**K**I**T**E**SS**D**---I**C**K**S**IYD**E**IL**G**CF**Y**FL**N**DE**E**LS**T**IS**D**VF**N**
 C. a. 180 **E**FL**I**L**I**NA**N**LE**D**LS**O**T**E**W**S**SS**D**L**K**---I**C**K**S**V**D**EL**I**AL**T**OL**N**ET**D**EN**M**FT**I**S**N**V**S**P
 S. p. 118 **S**ECAL**EN**CL**P**V**K**Q**K**E**V**NS**S**V**L**EN**T**IN**V**CKAS**L**NR**E**ME**M**CF**E**L**G**L**I**LA**E**FS**I**S**E**TX**K**P

S. c. 217 **S**TS**Q**VE**L**EV**E**DS**E**SS**E**T**I**PS**K**KT**O**SL**N**NA**E**N**O**HR**H**Q**P**Q**S**S**K**IN**E**V**Y**ET**I**ME**F**
 K. l. 221 **S**AD**H**PK**V**L**E**V**I**N**T**LA**N**AE**V**EH**O**LD**M**ST**E**EE-----S**Q**RA**L**P**Q**IE**D**EV**R**LE**V**
 C. a. 237 **NA**Q**D**LE**I**IT**D**IN**T**LA**N**AE**V**ST**S**GG**O**DD**V**N-----MD**V**Q**U**IDS**E**ST**S**FN**E**I
 S. p. 179 **S**TAE**V**EA**L**Q**I**EL**A**K**O**Q**E**VS**T**SS**S**IP**S**TD**N**---V**P**T**G**TS**I**LS**A**GR**E**VT**A**L

D

Homology of Bem1p binding region

```

S . g . 774 -----N I S S R I P T H A T E A V K N F O D E I K A N S E I S N T H N N I - S - P I T T K I Y O R
K . l . 789 -----D P V I L S I C E A R D I Q A I K R S E A S - V I L K V E Y O R
C . a . 746 T P D - V A I E L L Y K S T E I S E P I D I N A C T E Y N C I Q I K I S O I T S N T V A D D I - N I S E L E Y E L
S . p . 768 S V R N T T I N V I R L R L E V G L V E V V A H O I T E P E L A R V S K I K L C I I K O A N P P R V A L K V I
-----
E . c . 822 E D E D P V V I C S E E S W N V A E M A -----G N N E R F L N R I Y -
K . l . 723 E D E D P V V I E S D D N Y V I N O I K -----E S N E R L I S T V -
C . m . 804 E D E D P V V I N G I D N G V L I D I S D P Y Q T S N E K S V T I V S -
S . p . 828 E D E D E I I I S R E V S L M A F E T C I I L M D P V V H N K G M D T V S L E G V V Y P

```

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Figure 10

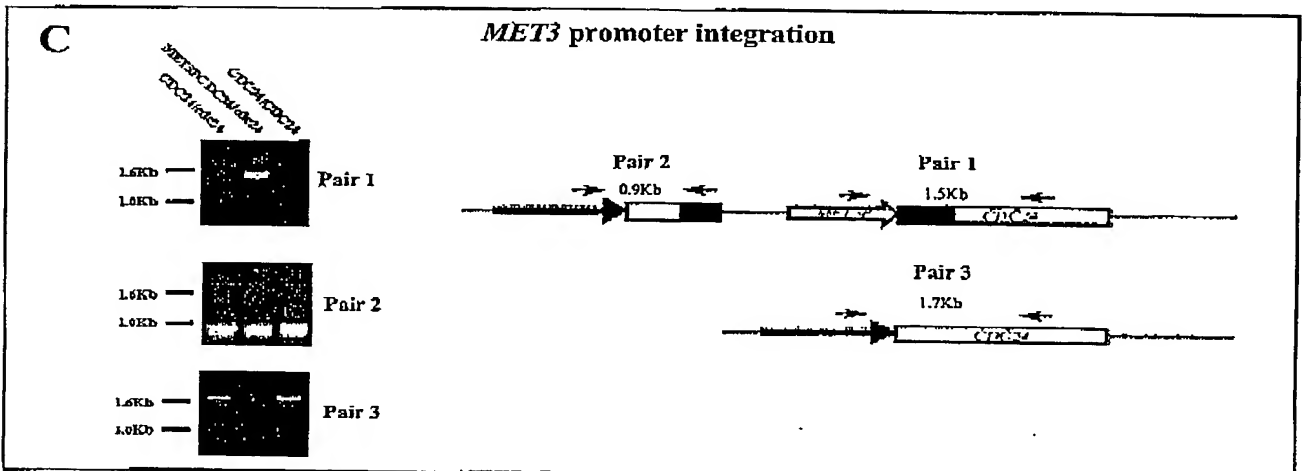
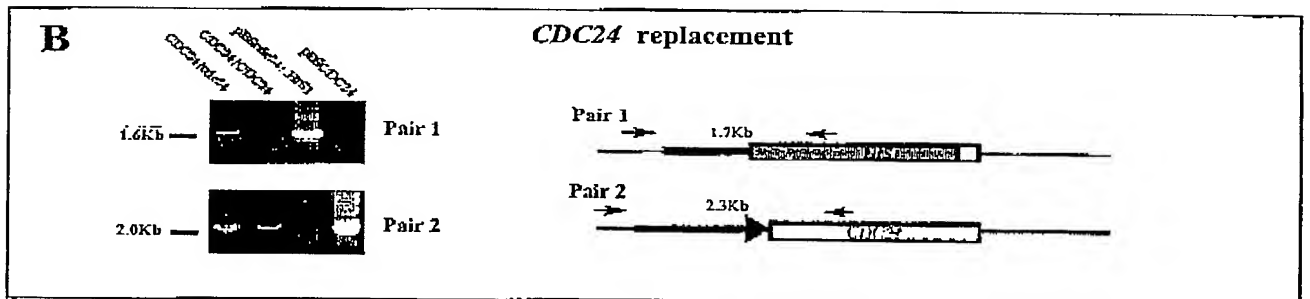
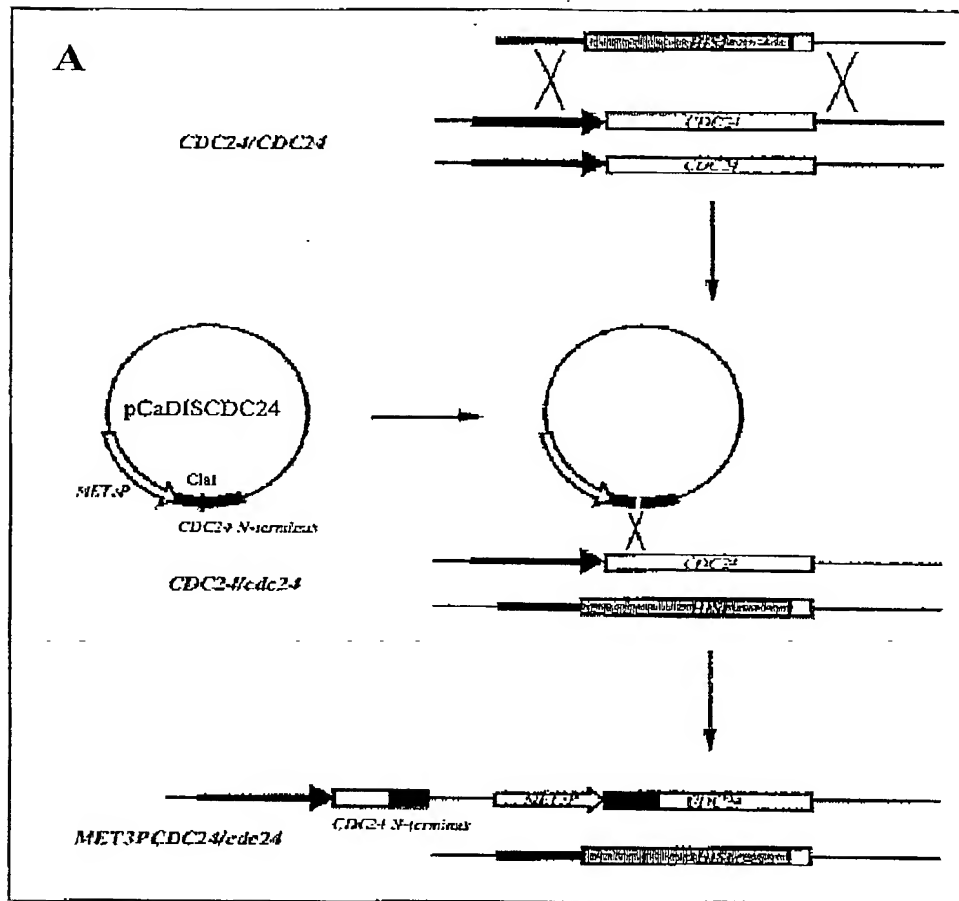
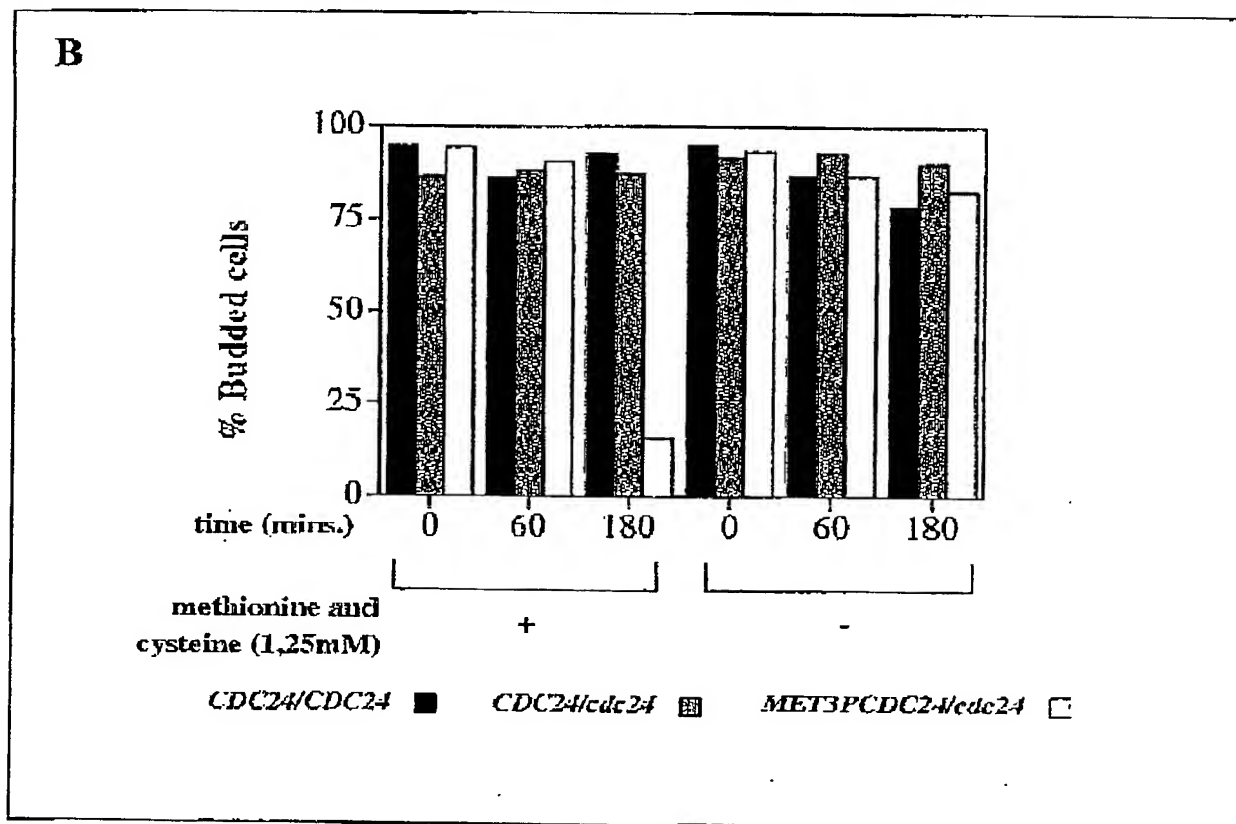
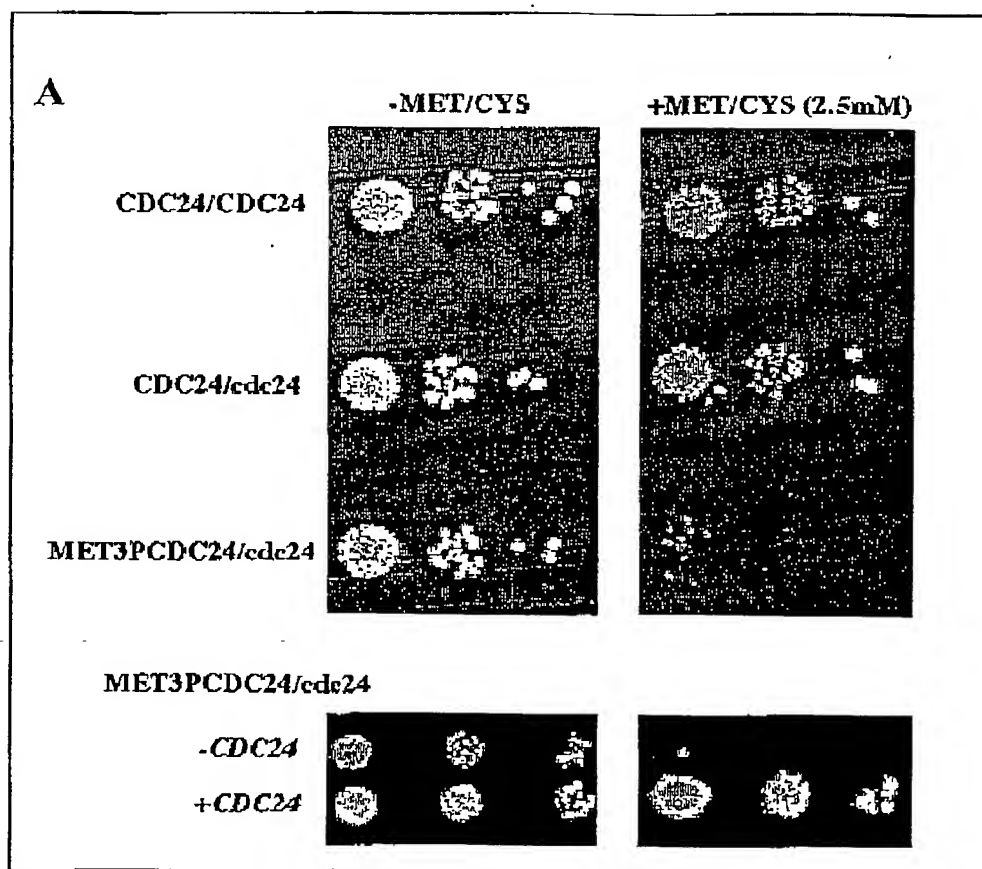


Figure 11



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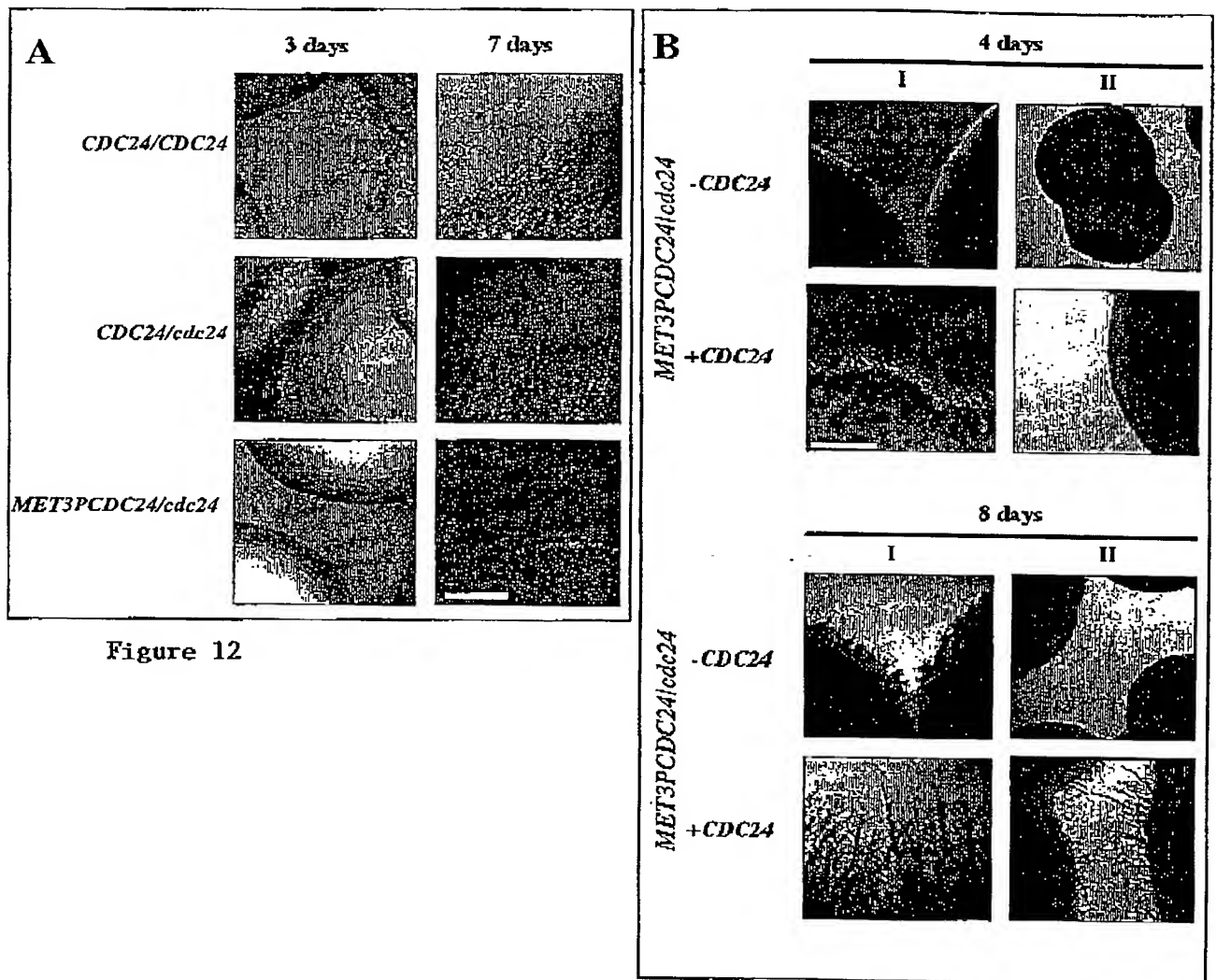


Figure 12

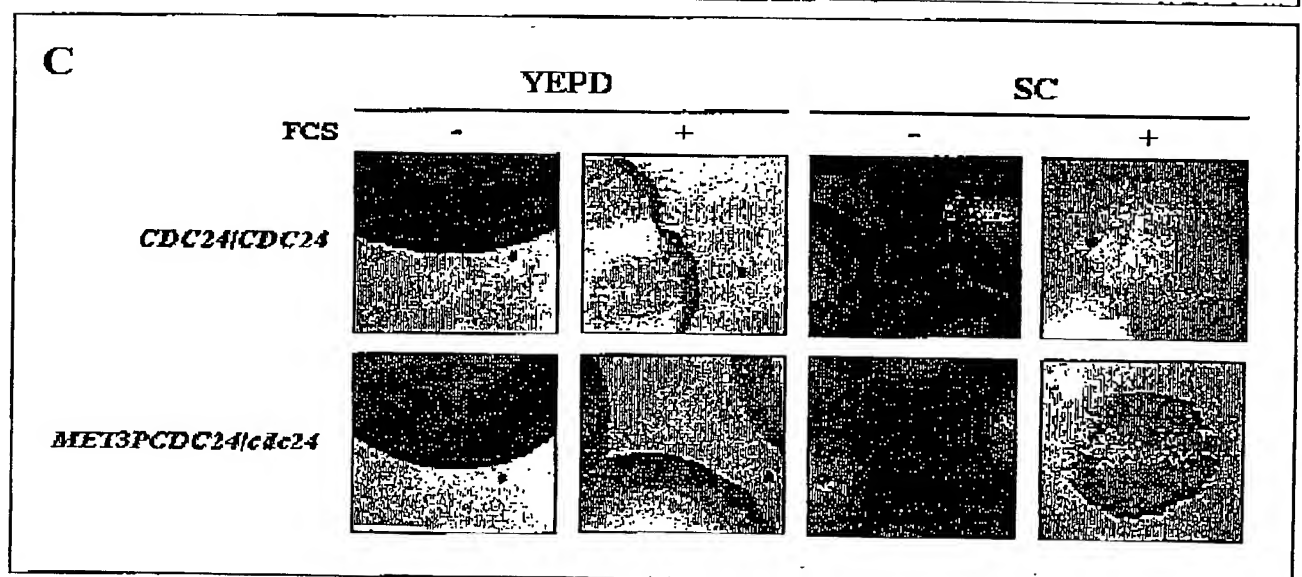


Figure 13

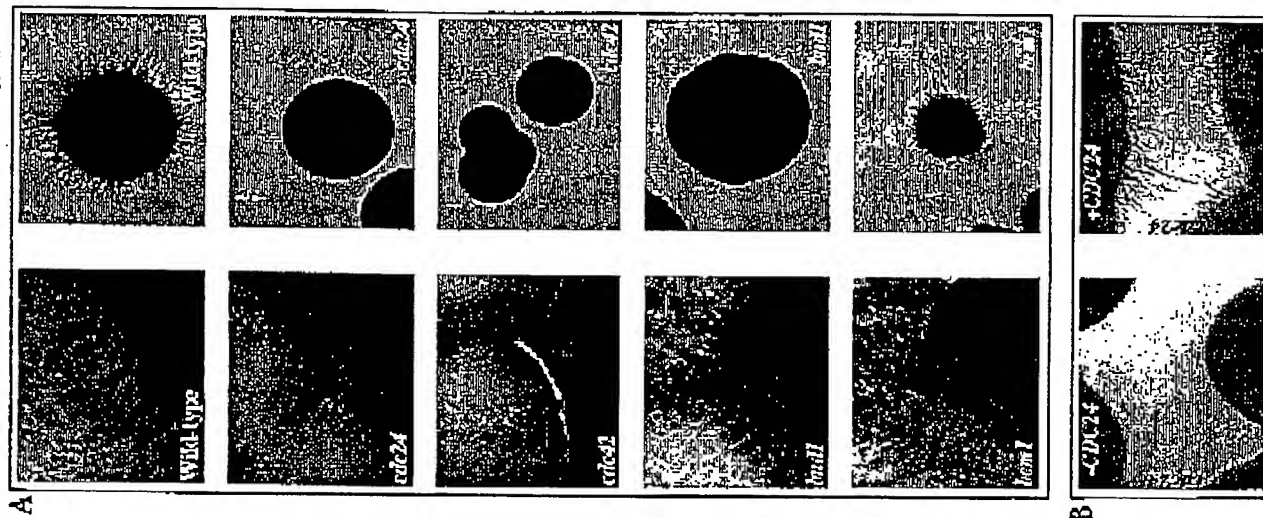
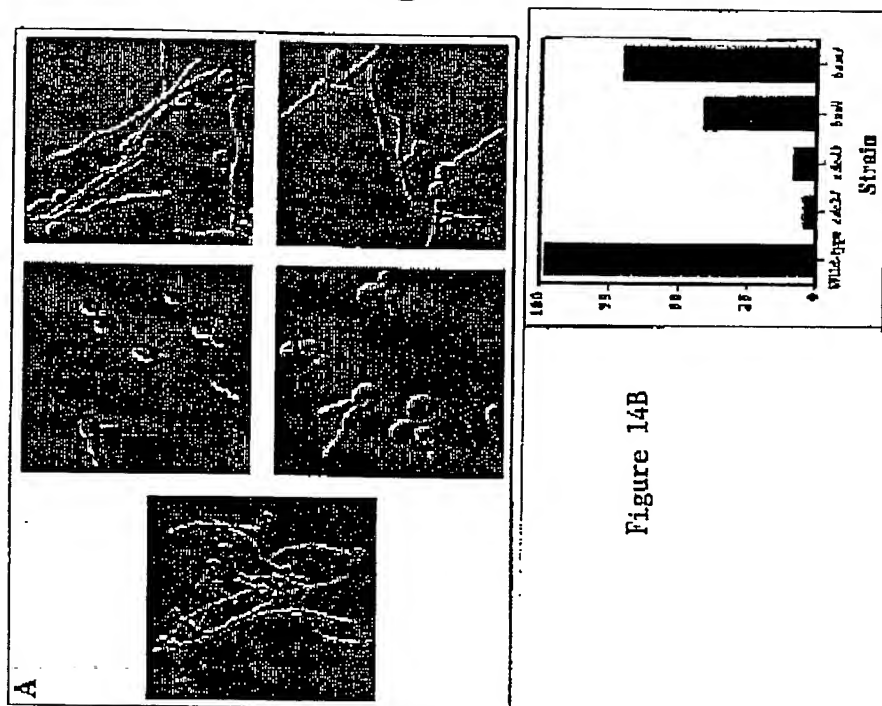


Figure 14B



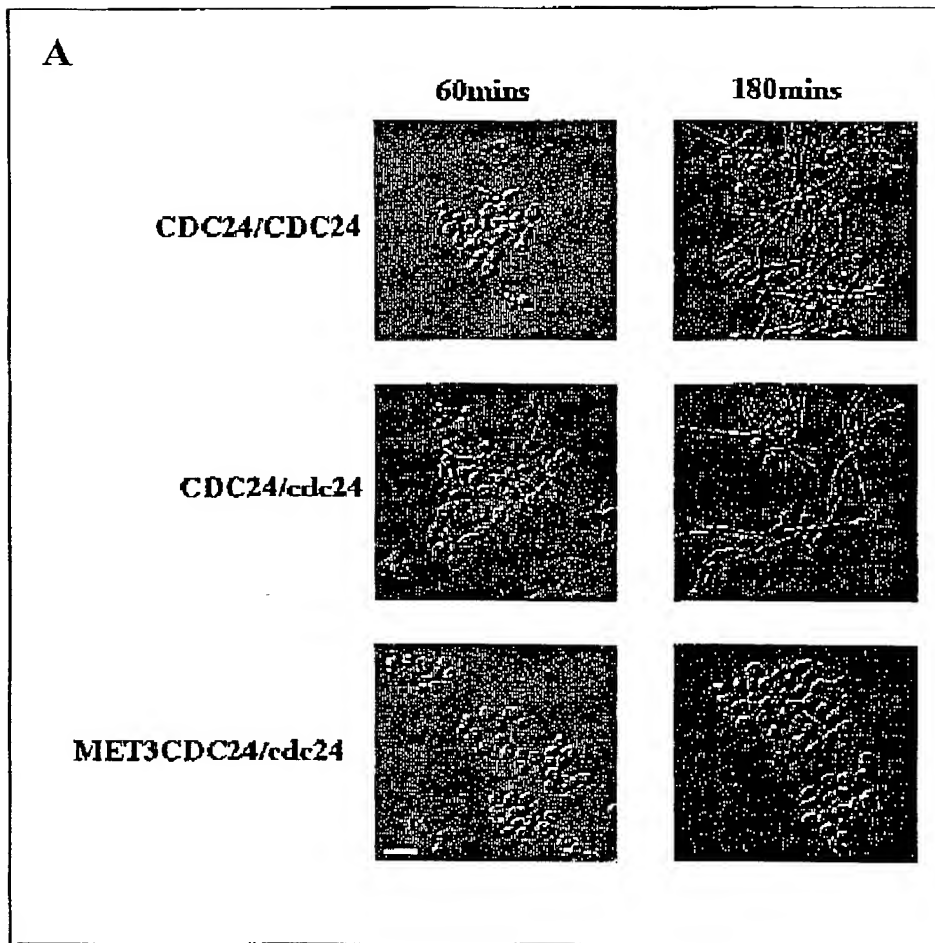
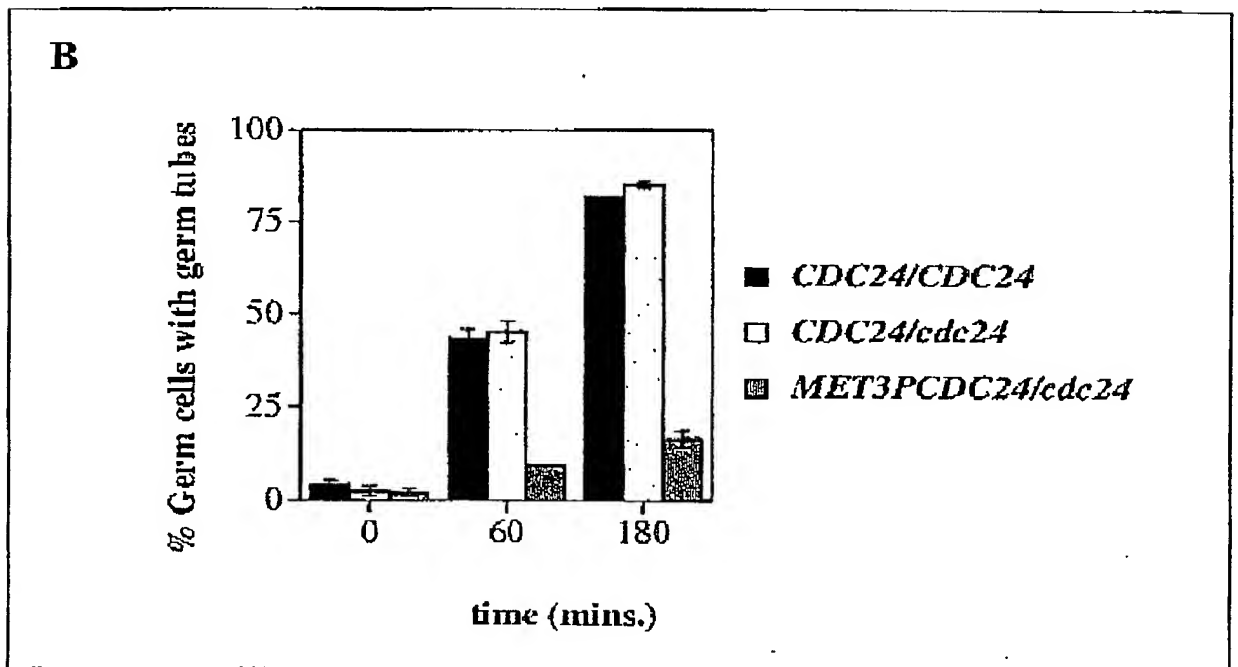
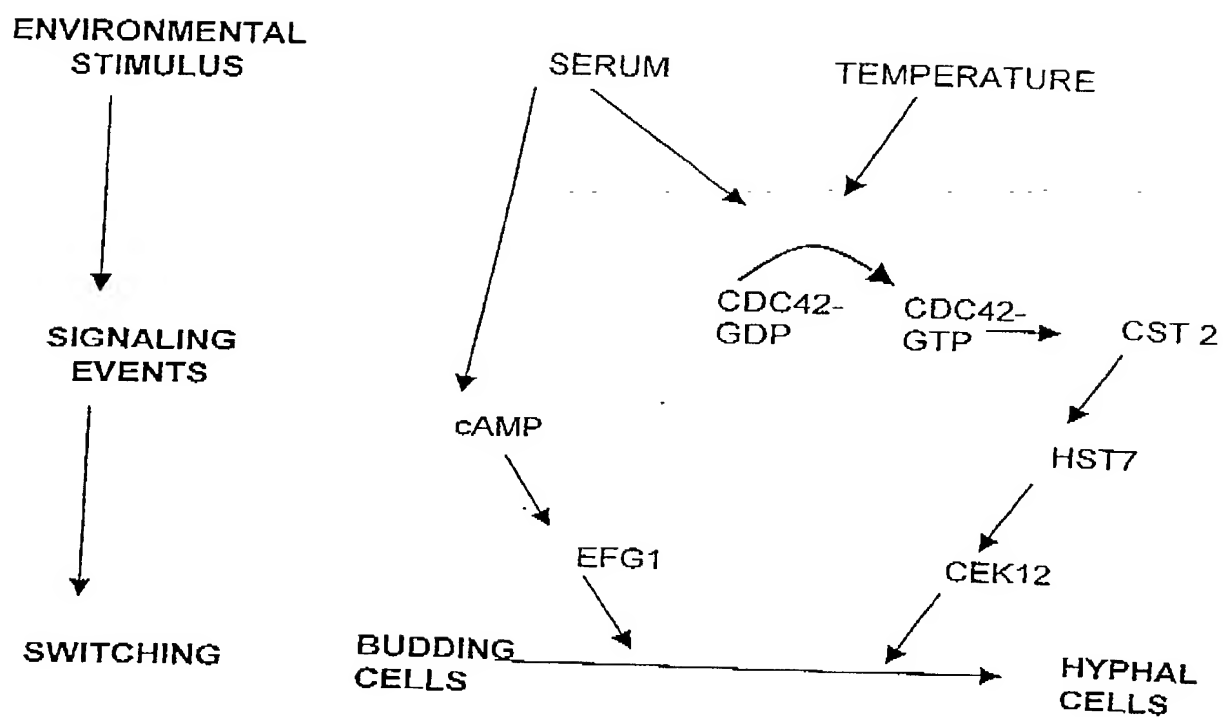


Figure 15



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Figure 16



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Figure 17

A. *cdc24* (wt)

5

SEQ. I.D. NO:1

DNA:

ccccctctgtatacttttcaactctgtgaagccgcaatttaaattaccggaatagcatctgacgatttgaaagtctgtaaaaatccatttatgactt
10 tatattgggctgcaagaaacactttgcatttaacgatgaggagcttttactatatccgacgttttgccaactcgacgtcccagctgggtcaaagt
gctagaagtagtagaaacgctaataatgaattccagc

SEQ. I.D. NO:2

Protein:

15 PLCILFNSVKPQFKLPVIASDDLKVCKKSIYDFILGCKKHFANDEELFTISDVFANSTSQ
LVKVLEVVEITLMNSS

B. *cdc24-m1*

20 SEQ. I.D. NO:3

DNA:

ccccctctgtatacttttcaactctgtgaagccgcaatttaaattaccggaatagcatttgacgatttgaaagtctgtaaaaatccatttatgactt
atatgggctgcaagaaacactttgcatttaacgatgaggagcttttactatatccgacgttttgccaactcgacgtcccagctgggtcaaagt
gctagaagtagtagaaacgctaataatgaattccagc

25

SEQ. I.D. NO:4

Protein:

PLCILFNSVKPQFKLPVIAFDDLKVCKKSIYDFILGCKKHFANDEELFTISDVFANSTSQ
LVKVLEVVEITLMNSS

30

C. *cdc24-m2*

5 SEQ. I.D. NO:5

DNA:

ccctctgtatacttttcaactctgtgaagccgcaatttaattaccggtaatagcatctggcgatttgaaagtctgtaaaaaatccatttatgacit
tatattgggctgcaagaaacactttgca11taacgatgaggagcttttactatatccgacgttttccaactcgacgtcccagctgggtcaaagt
gctagaagtagtagaaacgctaataatgaattccagc

10

SEQ. I.D. NO:6

Protein:

PLCILFNSVKPQFKLPVIASGDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ
LVKVLEVVEITLMNSS

15

D. *cdc24-m3*

SEQ. I.D. NO:7

DNA:

20 cccctctgtatacttttcaactctgtgaagccgcaatttaaattaccggtaatagcacctgacgatttgaaagtctgtaaaaaatccatttatgactt
tataattgggctgcaagaaacacittgcatttaacgatgaggagcttttactatatccgacgttttgccaactcgacgtcccagctgggtcaaagt
gctagaagtagtagaaacgctaattgaattccagc

SEQ. I.D. NO:8

25 Protein:

PLCILFNSVKPQFKLPVAPDDLKVCCKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ
LVKVLEVVEITLMNSS

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SEQ ID NO. 10

STE4 DNA sequence (wild-type)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCACAGTATATACACCACAAAGTCTACAGGA
 TATCTCTGCAGTGGAGGAGAAATTCAAAATAAATAGAGGGCCGCCAGACAGAGAGTAAACAGCTTCATGCTCAATAA
 ATRAAGCAAAACACAGATACAGATGCAAGCTTATTCAGATGGCCACAAAGTTACTTCGTTGACCAAAATAAGATC
 5 AACTTAAGCCAAATATCGTGTGAAAGGCCATAATAATAAATCTCAGATTTTCGGTGGAGTCCAGATTCAAACGTAT
 TTTGAGTGCAGTCAAGATGGCTTTAIGCTTATATGGGACAGTGCCTTCAGGTTTAAACAGACACCTATTCCATTAGATT
 CTCATATGGGTTCTTTCCCTGCGCTATTTCCGCCATCGAGTACTTTGGTAGCAAGCGCAGGATTAAACAATAACTGTACCATT
 TATAGAGTTTTCGAAAGAAACAGAGTAGCGCAAPACGTTGCGTCAATTTTCAAAGGACATACTTGCTATATTTCTGACAT
 TGAATTTACAGATACGACATATATTGACAGCAAGTGGGGATATGACATGTGCCCTGTGGGATATACCGAAAGCAAAGA
 10 GGGTGAGAGATATTTCTGACCATTTAGGTGATGTTTTGGCATTAGCTATTCCTGAAGAGCCAACTTAGAAATTCCTTCG
 AACACATTGCGTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCCCTCCCTGTACAAAGCTTTTA
 CGTTAACGATATGATATTAATGCACTTCGTTCTTTCAAAAGGAGGAGTGTTCGATTCTTCAGGAAATGACAAATGGTGGG
 TAAATATGATATGATTAAGGTGGGACTGTTCTATGCTACTTTTCTCTTTTTCGAGGTTATGAASAGCTACCCCTACG
 CCTACTTATATGCGAGCTAACATGGAGTACAATACCGCGCAATCGCCACAACTTTAAATCAACAAGCTCAAGCTATCT
 15 AACACAAACCAAGGGTGTGTTCTTTAGATTTTAGTGCATCTGGAAGATTGATGTAATCATGCTATACAGACATTGGTGTG
 TTGTGTGGGATCTATTAAAGGAGAGATTGTTGGAATATTAGAAAGTCATGGTGGCAGAGTCACTGGTGTGCGCTCGAGT
 CCAGATGGGTATGCTGATGACAGGTTTCATGGGACTCAACCTGAAATATGCTCTCCAGGTTATCAATAG

20

SEQ ID NO. 11

Ste4 Protein sequence (wild-type)

MAHQMDSITYSNVTCQYIQPQSLQDISAVEEEIQNKIEAARQESKQLHAQINKAKHKIQDASLFOMANKVTSLTKNKEI
 LKPNIVLKGENXKISDFRWSRDSKRILSASQDGFMLIWDASGLKQNAIFLDSQWVLSCAISPSTILVASAGLNMNCTI
 25 RYKERNVAQWVASIFKGHTCYISDIEFTDNAHILTASGDMTCALWDIPKAKRVREYSOHLGCVLALATFEENLENS
 TFASCGSDGYTYINDERSPSAVQSFYVNDSDINALRFFKDGMSIVAGSDNGATNMYDLRSDCSIATFSLFRGYEERTPT
 TYMAANMEYNTRQSPQELKSTSSSYLDNQGVVSLDFSASGRLMYSCYTDIGCVVWDVLKGEIVGKLEGHGGRVTGVRES
 DELAVCTGSWDSTMKIWSPGYQ

30

SEQ ID NO. 12

ste4-o15 DNA sequence (mutant)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCACAGTATATACACCACAAAGTCTACAGGA
 35 TATCTCTGCAGTGGAGGAGAAATTCAAAATAAATAGAGGGCCGCCAGACAGAGAGTAAACAGCTTCATGCTCAATTA
 ATRAAGCAAAACACAGATACAGATGCAAGCTTATTCAGATGGCCACAAAGTTACTTCGTTGACCAAAATAAGATC
 AACTTAAGCCAAATATCGTGTGAAAGGCCATAATAATAAATCTCAGATTTTCGGTGGAGTCCAGATTCAAACGT

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TTTGAGTGCAAGTCAAGATGGCTTTATGCTTATATGGGACAGTGCTTCAGGTTTAAACAGAACGCTATTCCATTAGAI
 CTCAATGGGTTCTTTCTGCGCTATTTTCGCCATCGAGTACTTTGGTAGCAAGCGCAGGATTAACAATAACTGTACCAI
 TATAGAGTTTTCGAAAGAAACAGAGTAGCGCAAAACGTTGCGTCAATTTTCAAGGACATACTTGCTATATTTCTGACA
 TGAATTTACAGATAACGCACATATATTGACAGCAAGTGGGGATATGACATGTGCCTTGTGGGATATACCGAAAGCAAAG
 5 GGGTGAGAGGATATTCTGACCATTAGGTGATGTTTTGGCATTAGCTATTTCCTGAAGAGCCAACTTAGAAAATTCTTC
 AACACATTTCGCTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCCGTCGCTGTACAAAGCTTTT
 CGTTAACGATAGTGATATTAATGCACTTCGTTTTTTTCAAAGACGGGATGTCGATTGTTGCAGGAAGTGACAATGGTGCG
 TAAATATGTATGATTTAAGGTCGGACTGTTCTATTGCTACTTTTTCTCTTTTCGAGGTTATGAAGAACGTACCCCTAC
 CCTACTTATATGGCAGCTAACATGGAGTACAATACCGCGCAATCGCCACAACTTTAAATCAACAGCTCAAGCTATC
 10 AGACAACCAAGGCGTTGTTTTCTTTAGATTTTAGTGATCTGGAAGATTGATGTACTCATGCTATACAGACATTGGTTGT
 TTGTGTGGGATCTATTAAAGGAGAGATTGTTGGAAAATTAGAAGGTCATGGTGGCAGAGTCACTGGTGTGCGCTCGAG
 CCAGATCGGCTTAGCTTATCTACAGGTCATGGGACTCAGCATGAATATATGGTCTCCAGGCTATCAATG

SEQ ID No. 13

15 Ste4-o15 Protein sequence (mutant)

MAHQMDSITYSNNVTQQYIQPQSLQDISAVEEEIQNKIEAARQESKQLHAQINKAKHKIQDASLFQMANKVTSLTKNK
 LKPNIVLKGNHNNKISDFRWSRDSKRILSASODGFMLIWDASGLKQNAIPLDSQWVLSCAISSSSTLVASAGLNNNCT
 RVSKENRVAQNVAIFKGHTCYISDIEFTDNAHILTAGDMTCALWDIPKAKRVRGYSOHLGQVLAALAIPEEPNLENS
 20 TFASCGSDGYTYIWDSSPSAVQSFYVNSDINALRFFKDGMSIVAGSDNGAINMYDLRSDCSIATFSLFRGYEERTF
 TYMAANMEYNATAQSPQTLKSTSSSYLONQGVVSLDPSASGRMLMYSCYTDIGCVVWDVLKGEIVGKLEGHGGRVTGVRS:
 DGLAVCTGSWDSTMKIWSPGYQ

SEQ ID NO. 14

25 ste4-o17 DNA sequence (mutant)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTCACCCAACAGTATATACAACCACAAAGTCTACAGGA
 TATCTCTGCAGTGGAGGAAGAAATTCAAATAAATAGAGGCCGCCAGACAAGAGAGTAAACAGCTTCATGCTCAAATP
 ATAAGCAAAACACAAGATACAAGATGCAAGCTTATTCCAGATGGCCACAAAGTTACTTCGTTGACCAAAAATAAGAI
 30 AACTTAAAGCCAAATATCGTGTTGAAAGGCCATAATAATAAATCTCAGATTTTCGGTGGAGTCGAGATTCAAACGTA
 TTTGAGTGCAAGTCAAGATGGCTTTATGCTTATATGGGACAGTGCTTCAGGTTTAAACAGAACGCTATTCCATTAGAI
 CTCAATGGGTTCTTTCTGCGCTATTTTCGCCATCGAGTACTTTGGTAGCAAGCGCAGGATTAACAATAACTGTACCAT
 TATAGAGTTTTCGAAAGAAACAGAGTAGCGCAAAACGTTGCGTCAATTTTCAAGGACATACTTGCTATATTTCTGACA
 TGAATTTACAGATAACGCACATATATTGACAGCAAGTGGGGATATGACATGTGCCTTGTGGGATATACCGAAAGCAAAG
 35 GGGTGAGAGGATATTCTGACCATTAGGTGATGTTTTGGCATTAGCTATTTCCTGAAGAGCCAACTTAGAAAATTCTTC
 AACACATTTCGCTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCCGTCGCTGTACAAAGCTTTT
 CGTTAACGATAGTGATATTAATGCACTTCGTTTTTTCAAAGACGGGATGTCGATTGTTGCAGGAAGTGACAATGGTGCG

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TAAATATGTATGATTTAAGGTCGGACTGTTCTATTGCTACTTTTTCTCTTTTCGAGGTTATGAAGAACGTACCCCTACC
CCTACTTATATGGCAGCTAACATGGAGTACAATACCGCGCAATCGCCACAAACTTTAAAATCAACLASCTCAAGCTATCT
AGACAACCAAGGCGCTGTTTCTTTAGATTTTAGTGCACTCTGGAAGATTGATGTACTCATGCTATACAGACATTGGTTGTG
TTGTGTGGGATGTATTAAAAGGAGAGATTGTTGGAAAATTAGAAGGTCATGGTGCCAGAGTCACTGGTGTGCGCTCGAGT
5 CCAGATGGGTTAGCTGTATGTACAGGTCATGGGACTCAACCATGAAAATATGGTCTCCAGGTTATCAATAG

SEQ ID No. 15

Ste4-o17 Protein sequence (mutant)

10 MAHQMDSITYSNNVTQQYIQPSLQDISAVEEEIQNKIEAARQESKQLHAQINKAKHKIQDASLFQMANKVTSLTKNKI
LKPNIVLKGHNKISDFRWSRDSKRILSASQDGFMLIWDSASGLKQNAIPLDSQWVLSCAISPSSTLVASAGLNNNCTI
RVSKENRVAQNVAIFKGHTCYISDIEFTDNAHILTAGDMTCALWDIPKAKRVREYSOHLGDVLAIAPEEPNLENSSI
TFASCGSDGYTYIWDSRSPSAVQSFYVNDSDINALRFFKDGMSIVAGSDNGAINMYDLRSDCSIATFSLFRGYERTPT
TYMAANMEYNTAQSPQTLKSTSSSYLDNQGAVSLDFSASGRMLMYSCYTDIGCVVWDVLKGEIVGKLEGHGGRVTGVASE
15 DGLAVCTGSWDSTMKIWSFGYQ

SEQ. I.D. No:16 refers to the epitope sequence "Tyr Pro Tyr Asp Val Pro Asp Tyr Ala".

SEQ. I.D. No:17 refers to TEV protease recognition sequence "Gln Asn Leu Tyr Phe Gln Gly"

SEQ. I.D. No:18 refers to peptide sequence "QFKLPVIAFDDLKVCKKSI".

SEQ. I.D. No:19 refers to peptide sequence "QFKLPVIASGDLKVCKKSI".

SEQ. I.D. No:20 refers to peptide sequence "QFKLPVIAPDDLKVCKKSI".

SEQ. I.D. No:21 refers to peptide sequence "QFKLPVIASDDLKVCKKSI".

SEQ. I.D. No:22 refers to peptide sequence "QYEFDVILSPELKVQMKT".